

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		Length	DB	ID		Description
	Score	Match %					
1	1724	100.0	329	6	ABU11876	<i>gum</i>	Abu11876 Thale cre
2	1703	98.8	327	8	ADN73841		Adn73841 Thale cre
3	1703	98.8	329	5	AAM50863		Aam50863 Arabidops
4	1698	98.5	327	3	AAG18223		Aag18223 Arabidops
5	1681	97.5	323	3	AAG18224		Aag18224 Arabidops
6	1330	77.1	250	3	AAG18225		Aag18225 Arabidops
7	113.5	6.6	549	6	ABU03090		Abu03090 Alpha amy
8	110.5	6.4	514	2	AAR78269		Aar78269 Bacillus
9	110.5	6.4	515	2	AAR72449		Aar72449 Bacillus
10	110.5	6.4	515	2	AAW31406		Aaw31406 Bacillus

RESULT 1

ABU11876

ID ABU11876 standard; protein; 329 AA.

XX

AC ABU11876;

XX

DT 13-FEB-2003 (first entry)

XX

DE Thale cress HY2 polypeptide.

XX

KW Thale cress; HY2; nucleus; phytochrome; apoprotein; cytoplasm;

KW heterologous transactivator; heterologous repressor; light response.

XX

OS Arabidopsis thaliana.

XX

PN WO200297137-A1.

XX

PD 05-DEC-2002.

XX

PF 29-MAY-2002; 2002WO-US017266.

XX

PR 29-MAY-2001; 2001US-0294463P.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Lagarius JC, Kochi T, Frankenberg N, Gambetta GA, Montgomery BL;

XX

DR WPI; 2003-041421/03.

DR N-PSDB; ABX50071.

XX

PT Transporting a polypeptide into the nucleus of a cell comprises using

PT light to transport a polypeptide attached to the apoprotein component of

PT a phytochrome into the nucleus.

XX

PS Example 1; Fig 3B; 102pp; English.

XX

CC The invention relates to a method for transporting a polypeptide into the

CC nucleus of a cell, comprising expressing a phytochrome comprising the

CC polypeptide attached to the apoprotein component of the phytochrome in a

CC cell, and exposing the cell to light where the phytochrome migrates from

CC the cytoplasm of the cell into the nucleus which transports the

CC polypeptide into the nucleus. The invention also relates to regulating

CC the transcription of a gene in response to light comprising expressing a

CC phytochrome containing a heterologous transactivator or repressor

CC attached to an apoprotein component of the phytochrome in a cell, and

CC exposing the cell to light where the phytochrome migrates from the

CC cytoplasm of the cell into the nucleus and the transactivator or

CC repressor alters expression of a gene in the nucleus. The methods are

CC used to transport a polypeptide into the nucleus of a cell or to regulate

CC the transcription of a gene in response to light. This sequence

CC represents the thale cress HY2 polypeptide used in the scope of the

CC invention

XX

SQ Sequence 329 AA;

Query Match 100.0%; Score 1724; DB 6; Length 329;

Best Local Similarity 100.0%; Pred. No. 9.7e-169;

Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MALSMEFGFSIGSCFKAPNPPVLISASPNKINFTLRRRKKRFLLRVSAVSYKEFAESALE 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MALSMEFGFSIGSCFKAPNPPVLISASPNKINFTLRRRKKRFLLRVSAVSYKEFAESALE 60

Qy     61 ETRKRIVLEPSHLQEKYSSMTGLDGKTELQMLAFKSSKIRLLRSMAIENETMQVDFDFAGF 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ETRKRIVLEPSHLQEKYSSMTGLDGKTELQMLAFKSSKIRLLRSMAIENETMQVDFDFAGF 120

Qy    121 MEPEYDTPIFCANFFTSTNVNIVVLDLNPLHQLTDQTDYQDKYYNKIMSIYHKYAETFPW 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 MEPEYDTPIFCANFFTSTNVNIVVLDLNPLHQLTDQTDYQDKYYNKIMSIYHKYAETFPW 180

Qy    181 GGKLTGESIKFFSPLVMWTRFSSSKEKHKALFSAFLEYQAWLEMTIQVREEMEPSHVRA 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGKLTGESIKFFSPLVMWTRFSSSKEKHKALFSAFLEYQAWLEMTIQVREEMEPSHVRA 240

Qy    241 NCEAQHKYLTWRAQKDPGHGLLKRLVGEAKAKELLRDFLFNGVDELGKTFIDYFPPEYQT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 NCEAQHKYLTWRAQKDPGHGLLKRLVGEAKAKELLRDFLFNGVDELGKTFIDYFPPEYQT 300

Qy    301 EDGTVSDKRSIIGKSYETRPWDLTGQFIG 329
        ||||||||||||||||||||||||||||
Db    301 EDGTVSDKRSIIGKSYETRPWDLTGQFIG 329
```

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1724	100.0	329	1	PFBS_ARATH	Q9sr43 arabidopsis
2	832.5	48.3	297	2	Q6E5A3	Q6e5a3 zea mays (m
3	592	34.3	240	2	Q8RZB6	Q8rzb6 oryza sativ
4	339.5	19.7	255	1	PEBB_NOSPU	Q93tm8 nostoc punc
5	330.5	19.2	255	2	Q6UR87	Q6ur87 fremyella d
6	292.5	17.0	245	1	PEBB_GLOVI	Q7nl65 gloeobacter
7	217.5	12.6	257	1	PEBB_SYNPY	Q02190 synechococc
8	216	12.5	257	1	PEBB_PROMM	Q7v585 prochloroco
9	215	12.5	257	1	PEBB_PROMA	Q9k4u5 prochloroco
10	209	12.1	262	1	PEBB_SYNPX	Q7u4p6 synechococc
11	202	11.7	244	1	PEBA_NOSPU	Q93tl6 nostoc punc
12	178	10.3	243	2	Q6UR88	Q6ur88 fremyella d
13	172.5	10.0	257	1	PEBB_PROMP	Q93sn7 prochloroco
14	158	9.2	236	1	PEBA_SYNPY	Q02189 synechococc
15	147	8.5	244	1	PEBA_GLOVI	Q7nl66 gloeobacter
16	145	8.4	235	1	PEBA_SYNPX	Q7u4p7 synechococc
17	136	7.9	236	1	PEBA_PROMP	Q93sn8 prochloroco
18	135	7.8	249	1	PEBA_PROMM	Q7v586 prochloroco
19	133.5	7.7	267	2	Q7XY33	Q7xy33 griffithsia

RESULT 1

PFBS_ARATH

ID PFBS_ARATH STANDARD; PRT; 329 AA.
AC Q9SR43; Q8L8Q6; Q9SS72;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Phytochromobilin:ferredoxin oxidoreductase, chloroplast precursor
DE (EC 1.3.7.4) (Phytochromobilin synthase) (PFB synthase) (PPhiB
DE synthase).
GN Name=HY2; OrderedLocusNames=At3g09150; ORFNames=F3L24.1, MZB10.18;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21124703; PubMed=11226195;
RA Kohchi T., Mukougawa K., Frankenberg N., Masuda M., Yokota A.,
RA Lagarias J.C.;
RT "The arabidopsis HY2 gene encodes phytochromobilin synthase, a
RT ferredoxin-dependent biliverdin reductase.";
RL Plant Cell 13:425-436(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713; DOI=10.1038/35048706;
RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisine N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:820-822(2000). *Dec 1998 2000*

RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
 RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
 RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
 RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
 RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
 RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
 RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 RT genome.";
 RL Science 302:842-846(2003).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.A.;
 RT "Full-length cDNA from Arabidopsis thaliana.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Catalyzes the two-electron reduction of biliverdin IXa
 CC to the tetrapyrrole chromophore phytochromobilin (PPhIB).
 CC -!- CATALYTIC ACTIVITY: (3Z)-phytochromobilin + oxidized ferredoxin =
 CC biliverdin IX-alpha + reduced ferredoxin.
 CC -!- SUBCELLULAR LOCATION: Chloroplast.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9SR43-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9SR43-2; Sequence=VSP_008970;
 CC Note=No experimental confirmation available;
 CC -!- SIMILARITY: Belongs to the HY2 family.
 CC -!- CAUTION: Ref.2 (AAD56331) sequence differs from that shown due to
 CC erroneous gene model prediction.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB045112; BAB33374.1; -.
 DR EMBL; AC011436; AAF14017.1; -.
 DR EMBL; AC009326; AAD56331.1; ALT_SEQ.
 DR EMBL; AY099706; AAM20557.1; -.
 DR EMBL; AY128900; AAM91300.1; -.
 DR EMBL; AY088874; AAM67180.1; ALT_INIT.
 DR InterPro; IPR009249; Fe_bilin_red.
 DR Pfam; PF05996; Fe_bilin_red; 1.

KW Alternative splicing; Chloroplast; Oxidoreductase; Transit peptide.
 FT TRANSIT 1 ? Chloroplast (Potential).
 FT CHAIN ? 329 Phytochromobilin:ferredoxin
 FT oxidoreductase.
 FT VARSPLIC 75 76 Missing (in isoform 2).
 FT /FTId=VSP_008970.
 FT CONFLICT 39 39 K -> N (in Ref. 4).
 SQ SEQUENCE 329 AA; 38129 MW; 98727CD1778D973C CRC64;

Query Match 100.0%; Score 1724; DB 1; Length 329;
 Best Local Similarity 100.0%; Pred. No. 3e-127;
 Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALSMFEGFSIGSCFKAPNPPVLISASPNKINFTLRRRKKRFLLRVSAVSYKEFAESALE 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MALSMFEGFSIGSCFKAPNPPVLISASPNKINFTLRRRKKRFLLRVSAVSYKEFAESALE 60
 Qy 61 ETRKRIVLEPSHLQEKYSSMTGLDGKTELQMLAFKSSKIRLLRSMAIENETMQVDFDAGF 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 ETRKRIVLEPSHLQEKYSSMTGLDGKTELQMLAFKSSKIRLLRSMAIENETMQVDFDAGF 120
 Qy 121 MEPEYDTPIFCANFFTSTNVNIVVLDLNPLHQLTDQTDYQDKYYNKIMSIYHKYAETFPW 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 MEPEYDTPIFCANFFTSTNVNIVVLDLNPLHQLTDQTDYQDKYYNKIMSIYHKYAETFPW 180
 Qy 181 GGKLTGESIKFFSPLVMWTRFSSSKEKHKALFSAFLEYQAWLEMTIQVREEMEPSHVRA 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 GGKLTGESIKFFSPLVMWTRFSSSKEKHKALFSAFLEYQAWLEMTIQVREEMEPSHVRA 240
 Qy 241 NCEAQHKYLTWRAQKDPGHGLLKRLVGEAKAKELLRDFLFNGVDELGKTTFIDYFPEYQT 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 NCEAQHKYLTWRAQKDPGHGLLKRLVGEAKAKELLRDFLFNGVDELGKTTFIDYFPEYQT 300
 Qy 301 EDGTVSDKRSIIGKSYETRPWDLTGQFIG 329
 ||||||||||||||||||||
 Db 301 EDGTVSDKRSIIGKSYETRPWDLTGQFIG 329

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	210.5	12.2	257	2	B46448	hypothetical prote
2	158	9.2	236	2	S31058	hypothetical prote
3	157	9.1	256	2	A46448	orf236 3' of cpeB
4	121.5	7.0	245	2	AD2269	hypothetical prote
5	110.5	6.4	549	1	A54541	alpha-amylase (EC
6	105.5	6.1	248	2	S76709	hypothetical prote
7	105	6.1	548	1	ALBSF	alpha-amylase (EC
8	104.5	6.1	549	1	A24549	alpha-amylase (EC
9	102.5	5.9	311	2	T30905	hypothetical prote
10	95.5	5.5	595	2	B97866	DNA primase (EC 2.
11	95.5	5.5	1125	1	F70177	transcription-repa
12	95	5.5	574	2	B35149	ipaH protein - Shi
13	94.5	5.5	649	2	T33741	DNA-binding protei
14	94	5.5	1452	2	A97323	DNA polymerase III
15	93.5	5.4	374	2	H70415	conserved hypothet
16	93.5	5.4	386	2	G86652	GTP-binding protei
17	93.5	5.4	2819	2	A90551	conserved

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1724	100.0	329	10	US-09-870-406A-33	Sequence 33, Appl
2	1724	100.0	329	10	US-09-870-406A-34	Sequence 34, Appl
3	1724	100.0	329	10	US-09-870-406A-55	Sequence 55, Appl
4	1724	100.0	329	14	US-10-159-901-33	Sequence 33, Appl
5	1724	100.0	329	14	US-10-159-901-34	Sequence 34, Appl
6	1724	100.0	329	14	US-10-159-901-55	Sequence 55, Appl
7	687	39.8	260	15	US-10-424-599-273255	Sequence 273255,
8	655.5	38.0	275	16	US-10-437-963-174730	Sequence 174730,
9	549	31.8	318	15	US-10-424-599-254892	Sequence 254892,
10	339.5	19.7	255	10	US-09-870-406A-54	Sequence 54

Database : Issued Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	110.5	6.4	514	3	US-09-182-859-6	Sequence 6, Appli
2	110.5	6.4	514	3	US-09-264-097-8	Sequence 8, Appli
3	110.5	6.4	514	4	US-09-672-459-6	Sequence 6, Appli
4	110.5	6.4	514	4	US-10-186-042-6	Sequence 6, Appli
5	110.5	6.4	515	3	US-09-291-023A-17	Sequence 17, Appl
6	110.5	6.4	515	4	US-09-537-168-8	Sequence 8, Appli
7	110.5	6.4	515	4	US-09-540-715A-17	Sequence 17, Appl
8	110.5	6.4	549	1	US-08-720-899-6	Sequence 6, Appli
9	110.5	6.4	549	1	US-08-459-610-6	Sequence 6, Appli
10	110.5	6.4	549	2	US-08-343-804-6	Sequence 6, Appli
11	110.5	6.4	549	2	US-08-687-399-6	Sequence 6, Appli
12	110.5	6.4	549	2	US-08-600-908A-6	Sequence 6, Appli
13	110.5	6.4	549	3	US-08-683-838A-6	Sequence 6, Appli
14	110.5	6.4	549	4	US-09-636-252A-6	Sequence 6, Appli